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(71) Applicant ( <i>for all designated States except US</i> ): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).  (72) Inventors; and (75) Inventors/Applicants ( <i>for US only</i> ): HE, Wei, Wu [CN/US]; 6225 Free Ston Court, Columbia, MD 21045 (US). HUDSON, Peter, L. [US/US]; 19041 High Stream Drive, Germantown, MD 20874 (US). ADAMS, Mark, D. [US/US]; 15205 Dufief Avenue, North Potomac, MD 20878 (US).  (74) Agents: OLSTEIN, Elliot, M. et al.; Carella, Byrne, Bain, Gilfillan, Cécchi, Stewart & Olstein, 6 Becker Farm Road, Roseland, NJ 07068 (US).		Published <i>With international search report.</i>	

(54) Title: TGF- $\beta$ 1, ACTIVIN RECEPTORS 1 AND 3

(57) Abstract

Polynucleotides encoding TAR-1 and TAR-3 receptor polypeptides, as well as such polypeptides, antibodies and antagonists against such polypeptides are disclosed. Also disclosed is a procedure for producing such polypeptides by recombinant techniques. Use of agonists and antagonists for therapeutic purposes, for example, to inhibit growth of cells and to treat lung and liver fibrosis is also disclosed.

**TGF- $\beta$ 1, ACTIVIN RECEPTORS 1 AND 3**

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the use of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides. More particularly, the polypeptide of the present invention is TGF- $\beta$ 1, Activin Receptors 1 and 3, sometimes hereinafter referred to as "TAR-1 and TAR-3". The invention also relates to inhibiting the action of such polypeptides.

The cloning of TGF- $\beta$ 1 and the resultant elucidation of its precursor structure (Derynck, et al., Nature, 316:701-705 (1985)) have led to the identification of at least four other forms of TGF- $\beta$  and the definition of a larger gene family comprising many other structurally related, but functionally distinct, regulatory proteins.

There are now many polypeptides that belong to the TGF- $\beta$  supergene family by virtue of amino acid homologies, particularly with respect to the conservation of seven of the nine cysteine residues of TGF- $\beta$  among all known family members. These include the mammalian inhibins (Mason, et al., Nature, 318:659-663 (1985)) and activins (Ling, et al., Nature, 279:782 (1986)), and mullerian inhibitory substance (Cate, et al., Cell, 45:685-698 (1986)), as well as the

Commun., 142:1095-1103 (1987)), and early embryonic development (Green and Smith, Nature, 347:391-394 (1990)). Activin has also been shown to suppress androgen production (Hsueh et al., PNAS, 84:5082-5086 (1987)), therefore activin decreases follicular size and may lead to female infertility (Woodruff et al., Endocrinol., 127:3196-3205 (1990)).

There are three activins (A, B, and AB), comprising different combinations of two closely-related beta sub-units, (Mason, A.J., et al., Nature, 318:659-663 (1985)). Activins impinge on a much broader spectrum of cells than inhibins, however, in those systems in which both proteins are functional, they have opposing biological effects. The mechanistic basis for this antagonism is unknown.

Cross-linking of labeled TGF- $\beta$  to membrane receptors has revealed three distinct classes of integral cell membrane components that bind TGF- $\beta$  (Massague, J., Biol. Chem., 260:7059-7066 (1985)). Class I components are 65 Kd in all species, whereas Class II components range from 85 Kd in rodent cells to 95 Kd in monkey and human cells to 110 Kd in chicken cells. Most frequently, all three classes of these binding proteins coexist on cells.

Type I and II TGF- $\beta$  receptor components, like most growth factor receptors, are glycoproteins. The type III protein is a proteoglycan consisting predominantly of heparin sulfate glycosaminoglycan chains with a smaller amount of chondroitin or dermatan sulfate attached to a core protein of about 100-140 Kd. The binding site for TGF- $\beta$  resides in this core protein (Cheifetz, et al., J. Biol. Chem., 263:16904-16991 (1988)).

An isolated TGF- $\beta$  supergene family receptor polypeptide has been disclosed in U.S. Patent No. 5,216,126. However, this receptor polypeptide has approximately 75% sequence identity with the mature human inhibin/activin receptor sequence. A protein designated as an "activin receptor" has been expression-cloned (Mathews and Vale, Cell, 65:1-20

(1991)), however, it does not appear to be a mammalian receptor in that it is a serine kinase.

In accordance with one aspect of the present invention, there are provided novel polypeptides which have been identified as TAR-1 and TAR-3 receptors, as well as fragments, analogs and derivatives thereof. The receptor polypeptides of the present invention are of human origin.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such receptor polypeptides.

In accordance with yet a further aspect of the present invention, there is provided a process for producing such receptor polypeptides by recombinant techniques.

In accordance with yet a further aspect of the present invention, there are provided processes for utilizing such receptor polypeptides, or polynucleotides encoding such receptor polypeptides for therapeutic purposes, for example, to determine the extent of the receptors in the cells of a patient, to measure all bindable forms of activin and TGF- $\beta$  and to screen for receptor antagonists and/or agonists to the TAR-1 and TAR-3 receptors.

In accordance with another aspect of the present invention there is provided a process of using such antagonists to treat liver and lung fibrosis.

In accordance with another aspect of the present invention there is provided a process of using such agonists for inhibiting proliferation of HIV virus and inhibiting the growth of cancer cells.

In accordance with yet a further aspect of the present invention, there are provided antibodies against such receptor polypeptides.

These and other aspects of the present invention should be apparent to those skilled in the art from the teachings herein.

The following drawings are illustrative of embodiments of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

Figure 1 is a cDNA sequence and corresponding deduced amino acid sequence of the TAR-1 receptor polypeptide. The signal sequence of the receptor polypeptide is the first 15 amino acids indicated and the transmembrane portion is underlined.

Figure 2 is the cDNA sequence and corresponding deduced amino acid sequence of the TAR-3 receptor polypeptide wherein the first 21 amino acids represent the signal sequence and the transmembrane portion is underlined. The standard one-letter abbreviation for amino acids is used throughout the figures.

Figure 3 illustrates the amino acid sequence homology between TAR-1 and TAR-3 and rat type I TGF- $\beta$  receptor. Boxed areas indicate identical amino acids between the different sequences.

Sequencing inaccuracies are a common problem when attempting to determine polynucleotide sequences. Accordingly, the sequences of Figure 1 and 2 are based on several sequencing runs and the sequencing accuracy is considered to be at least 97%.

The receptors of the present invention have been putatively identified as a TAR-1 and TAR-3 receptor. This identification has been made as a result of amino acid sequence homology.

In accordance with an aspect of the present invention, there are provided isolated nucleic acid (polynucleotides) which encode for the mature receptor polypeptides having the deduced amino acid sequence of Figure 1 and Figure 2 or for the mature receptor polypeptides encoded by the cDNA of the clone deposited as ATCC Deposit No. 75843 and ATCC Deposit No. 75842 for TAR-1 and TAR-3, respectively, which were deposited on July 27, 1994.

The polynucleotide encoding for TAR-1 was discovered in a cDNA library derived from a human adult spleen. It is structurally related to the TGF- $\beta$  receptor family. It contains an open reading frame encoding a protein of 509 amino acid residues of which approximately the first 27 amino acids residues are the putative signal sequence such that the mature protein comprises 482 amino acids. TAR-1 exhibits the highest degree of homology to type I TGF- $\beta$  receptor with 49% identity and 67% similarity over a 503 amino acid stretch.

The polynucleotide encoding for TAR-3 was discovered in a cDNA library derived from a human placenta. It is also structurally related to the TGF- $\beta$  receptor family. It contains an open reading frame encoding a protein of about 503 amino acid residues of which approximately the first 21 amino acids residues are the putative signal sequence such that the mature protein comprises 482 amino acids. TAR-3 also exhibits the highest degree of homology to type I TGF- $\beta$  receptor with 47% identity and 64% similarity over a 500 amino acid stretch.

The polynucleotides of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the mature receptor polypeptides may be identical to the coding sequence shown in Figure 1 and Figure 2 or that of the deposited clone(s) or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same, mature receptor polypeptides as the DNA of Figure 1 and Figure 2 or the deposited cDNA.

The polynucleotides which encode for the mature receptor polypeptides of Figure 1 and Figure 2 or for the mature receptor polypeptides encoded by the deposited cDNA(s) may include: only the coding sequence for the mature receptor

polypeptides; the coding sequence for the mature receptor polypeptides and additional coding sequence such as a leader or secretory sequence or a proprotein sequence; the coding sequence for the mature receptor polypeptides (and optionally additional coding sequence) and non-coding sequence, such as introns or non-coding sequence 5' and/or 3' of the coding sequence for the mature receptor polypeptides.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

The present invention further relates to variants of the hereinabove described polynucleotides which encode for fragments, analogs and derivatives of the polypeptides having the deduced amino acid sequence of Figure 1 and Figure 2 or the polypeptide encoded by the cDNA(s) of the deposited clone(s). The variant of the polynucleotides may be a naturally occurring allelic variant of the polynucleotides or a non-naturally occurring variant of the polynucleotides.

Thus, the present invention includes polynucleotides encoding the same mature receptor polypeptides as shown in Figure 1 and Figure 2 or the same mature receptor polypeptides encoded by the cDNA(s) of the deposited clone(s) as well as variants of such polynucleotides which variants encode for a fragment, derivative or analog of the receptor polypeptides of Figure 1 and Figure 2 or the receptor polypeptides encoded by the cDNA(s) of the deposited clone(s). Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

As hereinabove indicated, the polynucleotides may have a coding sequence which is a naturally occurring allelic variant of the coding sequences shown in Figure 1 and Figure 2 or of the coding sequences of the deposited clone(s). As known in the art, an allelic variant is an alternate form of

a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The present invention also includes polynucleotides, wherein the coding sequence for the mature receptor polypeptides may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the polypeptide. The polynucleotides may also encode for a proprotein which is the mature protein plus additional 5' amino acid residues. A mature protein having a prosequence is a proprotein and is an inactive form of the protein. Once the prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotides of the present invention may encode for mature receptor proteins, or for a receptor protein having a prosequence or for a receptor protein having both a prosequence and a presequence (leader sequence).

The polynucleotides of the present invention may also have the coding sequence fused in frame to a marker sequence which allows for purification of the receptor polypeptides of the present invention. The marker sequence may be a hexahistidine tag supplied by a pQE-9 vector to provide for purification of the mature receptor polypeptides fused to the marker in the case of a bacterial host, or, for example, the marker sequence may be a hemagglutinin (HA) tag when a mammalian host, e.g. COS-7 cells, is used. The HA tag corresponds to an epitope derived from the influenza

hemagglutinin protein (Wilson, I., et al., Cell, 37:767 (1984)).

The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% and preferably 70% identity between the sequences. The present invention particularly relates to polynucleotides which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode receptor polypeptides which retain substantially the same biological function or activity as the mature polypeptide encoded by the cDNA(s) of Figure 1 and Figure 2 or the deposited cDNA(s).

The deposit(s) referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited materials, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited materials, and no such license is hereby granted.

The present invention further relates to TAR-1 and TAR-3 receptor polypeptides which have the deduced amino acid sequence of Figure 1 and Figure 2 or which have the amino acid sequences encoded by the deposited cDNA(s), as well as fragments, analogs and derivatives of such polypeptide.

The terms "fragment," "derivative" and "analog" when referring to the receptor polypeptides of Figure 1 and Figure 2 or that encoded by the deposited cDNA(s), means receptor polypeptides which retain essentially the same biological function or activity as such polypeptides. Thus, an analog includes a proprotein which can be activated by cleavage of the proprotein portion to produce active mature receptor polypeptides.

The polypeptides of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analog of the receptor polypeptides of Figure 1 and Figure 2 or that encoded by the deposited cDNA(s) may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-

occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the TAR-1 and TAR-3 genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The polynucleotides of the present invention may be employed for producing receptor polypeptides by recombinant techniques. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies.

However, any other vector may be used as long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the E. coli. lac or trp, the phage lambda P<sub>1</sub> promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in E. coli.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the proteins.

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as E. coli, Streptomyces, Salmonella typhimurium; fungal cells, such as yeast; insect cells such as Drosophila and Sf9; animal cells such as CHO, COS or Bowes melanoma; plant cells, etc. The

selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and PCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, P<sub>L</sub> and trp. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast

cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation. (Davis, L., Dibner, M., Battey, J., Basic Methods in Molecular Biology, (1986)).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Transcription of the DNA encoding the receptor polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples including the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and

a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK),  $\alpha$ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include E. coli, Bacillus subtilis, Salmonella typhimurium and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, WI, USA). These pBR322 "backbone"

sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell, 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

The TAR-1 and TAR-3 receptor polypeptides can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography hydroxylapatite chromatography,

chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The receptor polypeptides of the present invention may be a naturally purified product, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. The polypeptides may also include an initial methionine residue.

The present invention also relates to detecting altered levels of expression of mRNA encoding TAR-1 and TAR-3 receptors. The overexpression of these genes or loss of expression is indicative of cancer or the risk of cancer. Assays employed to detect the expression of these nucleic acid sequences are well-known by those skilled in the art and include, for example, nucleic acid probe hybridization, PCR and Southern blot analysis. In the hybridization technique, a sample is derived from a host and analyzed to determine whether the sample contains altered levels of TAR receptor gene expression.

TAR-1 and TAR-3 receptor polypeptides are useful in radio-receptor assays to measure all bindable (and active) forms of a TGF supergene family member such as activin. Such an assay would be specific for activin and would be conducted using the naturally purified or recombinant TAR-1 and TAR-3 receptors as the receptor element.

In addition, TAR-1 and TAR-3 receptor polypeptides are useful for screening for compounds that bind to them and have TGF supergene family biological activity as defined above. Preferably, these compounds are small molecules such as

organic or peptide molecules that exhibit one or more of the desired activities of a TGF supergene family member such as activin. Screening assays of this kind are conventional in the art, and any such screening procedure may be employed, whereby the test sample is contacted with the TAR-1 or TAR-3 receptor herein and the extent of binding and biological activity of the bound molecules is determined.

TAR-1 and TAR-3 receptor polypeptides are additionally useful in affinity purification of TGF supergene family members that bind TAR-1 and TAR-3 receptors and in purifying antibodies thereto. The receptor is typically coupled to an immobilized resin such as Affi-Gel 10 (Bio-Rad, Richmond, CA) or other such resins (support matrices) by means well-known in the art. The resin is equilibrated in a buffer and the preparation to be purified is placed in contact with the resin, whereby the molecules are selectively adsorbed to the receptor on the resin. The resin is then sequentially washed with suitable buffers to remove non-adsorbed material, including unwanted contaminants, from the mixture to be purified, using, for an activin mixture, e.g., 100mM glycine, pH 3, and 0.1% octyl  $\beta$ -glucoside. The resin is then treated so as to elute the compound using a buffer that will break the bond between the compound and receptor.

The TAR-1 and TAR-3 receptors of the present invention may also be employed in a process for screening for antagonists and/or agonists for the receptors. As an example, mammalian cells or membrane preparations expressing either the TAR-1 or TAR-3 receptor would be incubated with labeled ligand in the presence of compound. The ability of the compound to enhance or block this interaction could then be measured. Alternatively, the response of a known second messenger system following interaction of ligand and receptor would be measured compared in the presence or absence of the compound. Such second messenger systems include but are not

limited to, cAMP guanylate cyclase, ion channels or phosphoinositide hydrolysis.

Other screening techniques include the use of cells which express the receptors (for example, transfected CHO cells) in a system which measures extracellular pH changes caused by receptor activation, for example, as described in Science, volume 246, pages 181-296 (October 1989). For example, potential agonists or antagonists may be contacted with a cell which expresses the receptors and a second messenger response, e.g. signal transduction or pH changes, may be measured to determine whether the potential agonist or antagonist is effective.

Another such screening technique involves introducing RNA encoding the receptors into *xenopus* oocytes to transiently express the receptor. The receptor oocytes may then be contacted in the case of antagonist screening with the receptor ligand and a compound to be screened, followed by detection of inhibition of a calcium signal.

Another screening technique involves expressing the TAR-1 or TAR-3 receptor in which the receptor is linked to a phospholipase C or D. As representative examples of such cells, there may be mentioned endothelial cells, smooth muscle cells, embryonic kidney cells, etc. The screening for an antagonist or agonist may be accomplished as hereinabove described by detecting activation of the receptor or inhibition of activation of the receptor from the phospholipase second signal.

A potential antagonist is an antibody, or in some cases an oligonucleotide, which binds to the TAR-1 and TAR-3 receptors but does not elicit a second messenger response such that the activity of the receptors is prevented.

Potential antagonists also include proteins which are closely related to the ligand of the receptors, i.e. a fragment of the ligand, which have lost biological function

and when binding to the TAR-1 and TAR-3 receptors, elicit no response.

A potential antagonist also includes an antisense construct prepared through the use of antisense technology. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes for the mature polypeptides of the present invention, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix -see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al, Science, 241:456 (1988); and Dervan et al., Science, 251: 1360 (1991)), thereby preventing transcription and the production of TAR-1 and TAR-3 receptors. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the receptors (antisense - Okano, J. Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the receptors.

Another potential antagonist is a small molecule which binds to the TAR-1 and/or TAR-3 receptors, making them inaccessible to ligands such that normal biological activity is prevented. Examples of small molecules include but are not limited to small peptides or peptide-like molecules.

Potential antagonists also include a soluble form of a TAR-1 and TAR-3 receptors, e.g. a fragment of the receptor, which binds to the ligand and prevents the ligand from interacting with membrane bound receptors. These soluble

fragments bind to TGF- $\beta$  and/or activin and prevent binding to membrane-bound receptors.

TGF- $\beta$  stimulates fibroblasts to migrate to a site of injury, proliferate and produce collagen, TGF- $\beta$  also inhibits collagen degradation. These excessive levels of collagen lead to liver and lung fibrosis. Accordingly, antagonists of TAR-1 and TAR-3 receptors will prevent liver and lung fibrosis.

The antagonists may also be employed to treat female sterility, since activin decreases follicle size and may lead to this disorder. The antagonists may be employed in a composition with a pharmaceutically acceptable carrier, e.g., as hereinafter described.

Agonists to the TAR-1 and TAR-3 receptors may be employed to activate these receptors and upregulate the functional application of TGF- $\beta$ . Since TGF- $\beta$  has been implicated in suppressing growth of cancerous cells, the activation of the TAR-1 and TAR-3 receptor may be employed to treat cancer. TGF- $\beta$  also inhibits growth and proliferation of the HIV virus and accordingly stimulating the TAR-1 and TAR-3 receptors treats HIV infection.

Agonists which stimulate these receptors also will upregulate activins and stimulate spermatogonial proliferation to treat male infertility.

The agonists and antagonists of the present invention may be employed in combination with a suitable pharmaceutical carrier. Such compositions comprise a therapeutically effective amount of the agonist or antagonist and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The formulation should suit the mode of administration.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of

the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

The pharmaceutical compositions may be administered in a convenient manner such as by the topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, the pharmaceutical compositions will be administered in an amount of at least about 10 µg/kg body weight and in most cases they will be administered in an amount not in excess of about 3 mg/Kg body weight per day. In most cases, the dosage is from about 10 µg/kg to about 1 mg/kg body weight daily, taking into account the routes of administration, symptoms, etc.

The TAR-1 and TAR-3 receptor polypeptides and agonists and antagonists which are polypeptides may also be employed in accordance with the invention by expression of the polypeptides *in vivo*, which is often referred to as "gene therapy".

For example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) encoding the TAR-1 and TAR-3 polypeptides *ex vivo*, with the engineered cells then being provided to a patient to be treated with the polypeptides. Such methods are well-known in the art. For example, cells may be engineered by procedures known in the art by use of a retroviral particle containing RNA encoding a polypeptide of the present invention.

Similarly, cells may be engineered *in vivo* for expression of a polypeptide *in vivo* by, for example, procedures known in the art. As known in the art, a producer cell for producing a retroviral particle containing RNA encoding the polypeptide of the present invention may be administered to a patient for engineering cells *in vivo* and expression of the polypeptide *in vivo*. These and other methods for administering a polypeptide of the present invention by such method should be apparent to those skilled in the art from the teachings of the present invention. For example, the expression vehicle for engineering cells may be other than a retrovirus, for example, an adenovirus which may be used to engineer cells *in vivo* after combination with a suitable delivery vehicle.

The sequences of the present invention are also valuable for chromosome identification. The sequence is specifically targeted to and can hybridize with a particular location on an individual human chromosome. Moreover, there is a current need for identifying particular sites on the chromosome. Few chromosome marking reagents based on actual sequence data (repeat polymorphisms) are presently available for marking chromosomal location. The mapping of DNAs to chromosomes according to the present invention is an important first step in correlating those sequences with genes associated with disease.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the cDNA(s). Computer analysis of the cDNA(s) is used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the primer will yield an amplified fragment.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular DNA to a particular chromosome. Using the present invention with the same oligonucleotide primers, sublocalization can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in an analogous manner. Other mapping strategies that can similarly be used to map to its chromosome include *in situ* hybridization, prescreening with labeled flow-sorted chromosomes and preselection by hybridization to construct chromosome specific-cDNA(s) libraries.

Fluorescence *in situ* hybridization (FISH) of a cDNA(s) clones to a metaphase chromosomal spread can be used to provide a precise chromosomal location in one step. This technique can be used with cDNA(s) as short as 500 or 600 bases; however, clones larger than 2,000 bp have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. FISH requires use of the clones from which the EST was derived, and the longer the better. For example, 2,000 bp is good, 4,000 is better, and more than 4,000 is probably not necessary to get good results a reasonable percentage of the time. For a review of this technique, see Verma et al., *Human Chromosomes: a Manual of Basic Techniques*, Pergamon Press, New York (1988).

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, for example, in V. McKusick, *Mendelian Inheritance in Man* (available on line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (coinheritance of physically adjacent genes).

Next, it is necessary to determine the differences in the cDNA(s) or genomic sequence between affected and

unaffected individuals. If a mutation is observed in some or all of the affected individuals but not in any normal individuals, then the mutation is likely to be the causative agent of the disease.

With current resolution of physical mapping and genetic mapping techniques, a cDNA(s) precisely localized to a chromosomal region associated with the disease could be one of between 50 and 500 potential causative genes. (This assumes 1 megabase mapping resolution and one gene per 20 kb).

The polypeptides, their fragments or other derivatives, or analogs thereof, or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The present invention also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides corresponding to a sequence of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, 1975, *Nature*, 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, *Immunology Today* 4:72), and the EBV-

hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention.

The present invention will be further described with reference to the following examples; however, it is to be understood that the present invention is not limited to such examples. All parts or amounts, unless otherwise specified, are by weight.

In order to facilitate understanding of the following examples certain frequently occurring methods and/or terms will be described.

"Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

"Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for

particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37°C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. et al., Nucleic Acids Res., 8:4057 (1980).

"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., et al., Id., p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units to T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

Unless otherwise stated, transformation was performed as described in the method of Graham, F. and Van der Eb, A., Virology, 52:456-457 (1973).

#### Example 1

##### Expression of Recombinant TAR-1 in COS cells

The expression of plasmid, TAR-1 HA is derived from a vector pcDNA(s)I/Amp (Invitrogen) containing: 1) SV40 origin of replication, 2) ampicillin resistance gene, 3) E.coli replication origin, 4) CMV promoter followed by a polylinker region, a SV40 intron and polyadenylation site. A DNA

fragment encoding the entire TAR-1 precursor and a HA tag fused in frame to its 3' end was cloned into the polylinker region of the vector, therefore, the recombinant protein expression is directed under the CMV promoter. The HA tag correspond to an epitope derived from the influenza hemagglutinin protein as previously described (I. Wilson, H. Niman, R. Heighten, A. Cherenson, M. Connolly, and R. Lerner, 1984, Cell 37, 767). The infusion of HA tag to our target protein allows easy detection of the recombinant protein with an antibody that recognizes the HA epitope.

The plasmid construction strategy is described as follows:

The DNA sequence encoding TAR-1, ATCC # 75843, was constructed by PCR on the original EST cloned using two primers: the 5' primer 5' GCGCGAAGCTTACAATGGTAGATGG AGTGAT 3' contains a Hind III site followed by 21 nucleotides of TAR-1 coding sequence including the initiation codon; the 3' sequence 5' GCGCGCTCGAGTCAGCGTAGTCTGGGACGTCGTATGG GTAACAGTCAGTTCAATTGT 3' contains complementary sequences to an Xho site, translation stop codon, HA tag and the last 20 nucleotides of the TAR-1 coding sequence (not including the stop codon). Therefore, the PCR product contains a Hind III site, TAR-1 coding sequence followed by HA tag fused in frame, a translation termination stop codon next to the HA tag, and an Xho site. The PCR amplified DNA fragment and the vector, pcDNA(s)I/Amp, were digested with Hind III and Xho I restriction enzyme and ligated. The ligation mixture was transformed into E. coli strain SURE (available from Stratagene Cloning Systems, 11099 North Torrey Pines Road, La Jolla, CA 92037) the transformed culture was plated on ampicillin media plates and resistant colonies were selected. Plasmid DNA was isolated from transformants and examined by restriction analysis for the presence of the correct fragment. For expression of the recombinant TAR-1, COS cells were transfected with the expression vector by DEAE-DEXTRAN

method. (J. Sambrook, E. Fritsch, T. Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Laboratory Press, (1989)). The expression of the TAR-1 HA protein was detected by radiolabelling and immunoprecipitation method. (E. Harlow, D. Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, (1988)). Cells were labelled for 8 hours with <sup>35</sup>S-cysteine two days post transfection. Culture media were then collected and cells were lysed with detergent (RIPA buffer (150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50mM Tris, pH 7.5). (Wilson, I. et al., Id. 37:767 (1984)). Both cell lysate and culture media were precipitated with a HA specific monoclonal antibody. Proteins precipitated were analyzed on 15% SDS-PAGE gels.

#### Example 2

##### Expression of Recombinant TAR-3 in COS cells

The expression of plasmid, TAR-3 HA is derived from a vector pCDNA(s)I/Amp (Invitrogen) containing: 1) SV40 origin of replication, 2) ampicillin resistance gene, 3) E.coli replication origin, 4) CMV promoter followed by a polylinker region, a SV40 intron and polyadenylation site. A DNA fragment encoding the entire TAR-3 precursor and a HA tag fused in frame to its 3' end was cloned into the polylinker region of the vector, therefore, the recombinant protein expression is directed under the CMV promoter. The HA tag correspond to an epitope derived from the influenza hemagglutinin protein as previously described (I. Wilson, H. Niman, R. Heighten, A Cherenson, M. Connolly, and R. Lerner, 1984, Cell 37, 767). The infusion of HA tag to our target protein allows easy detection of the recombinant protein with an antibody that recognizes the HA epitope.

The plasmid construction strategy is described as follows:

The DNA sequence encoding TAR-3, ATCC No. 75842, was constructed by PCR on the full-length TAR-3 clone using two primers: the 5' primer is 5' GCGCGAAGCTTACCATGACC TTGGGCTCCCCCA 3' contains a Hind III site followed by 22 nucleotides of TAR-3 coding sequence starting from the initiation codon; the 3' sequence 5' GCGCGTCTAGATCAAGCGTAG TCTGGGACGTCGTATGGGTAGTGAATCACTTTGGGCTTCTC 3' contains complementary sequences to an Xba I site, translation stop codon, HA tag and the last 21 nucleotides of the TAR-3 coding sequence (not including the stop codon). Therefore, the PCR product contains a Hind III site, TAR-3 coding sequence followed by HA tag fused in frame, a translation termination stop codon next to the HA tag, and an Xba I site. The PCR amplified DNA fragment and the vector, pcDNA(s)I/Amp, were digested with Hind III and Xba I restriction enzyme and ligated. The ligation mixture was transformed into E. coli strain SURE (available from Stratagene Cloning Systems, 11099 North Torrey Pines Road, La Jolla, CA 92037) the transformed culture was plated on ampicillin media plates and resistant colonies were selected. Plasmid DNA was isolated from transformants and examined by restriction analysis for the presence of the correct fragment. For expression of the recombinant TAR-3, COS cells were transfected with the expression vector by DEAE-DEXTRAN method. (J. Sambrook, E. Fritsch, T. Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Laboratory Press, (1989)). The expression of the TAR-3 HA protein was detected by radiolabeling and immunoprecipitation method. (E. Harlow, D. Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, (1988)). Cells were labelled for 8 hours with <sup>35</sup>S-cysteine two days post transfection. Culture media were then collected and cells were lysed with detergent (RIPA buffer (150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50mM Tris, pH 7.5). (Wilson, I. et al., Id. 37:767 (1984)). Both cell lysate and culture media were precipitated with a HA

specific monoclonal antibody. Proteins precipitated were analyzed on 15% SDS-PAGE gels.

Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, within the scope of the appended claims, the invention may be practiced otherwise than as particularly described.

## SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: HE, ET AL.
- (ii) TITLE OF INVENTION: TAR-1 and TAR-3
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
CECCHI, STEWART & OLSTEIN
- (B) STREET: 6 BECKER FARM ROAD
- (C) CITY: ROSELAND
- (D) STATE: NEW JERSEY
- (E) COUNTRY: USA
- (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 INCH DISKETTE
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE: Submitted herewith
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
- (A) APPLICATION NUMBER:
- (B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: FERRARO, GREGORY D.
- (B) REGISTRATION NUMBER: 36,134
- (C) REFERENCE/DOCKET NUMBER: 325800-132

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1539 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TACAATGGTA	GATGGAGTGA	TGATTCTTCC	TGTGCTTATC	ATGATTGCTC	TCCCCTCCCC	60
TAGTATGGAA	GATGAGAACG	CCAAGGTCAA	CCCCAAACTC	TACATGTGTG	TGTGTGAAGG	120
TCTCTCCTGC	GGTAATGAGG	ACCACTGTGA	AGGCCAGCAG	TGCTTTCCCT	CACTGAGCAT	180
CACCGATGGC	TTCCACTGCT	ACCAGAAAGG	CTGCTTCAG	GTTTATGAGC	AGGGAAAGAT	240
GACCTGTAAG	ACCCCGCCGT	CCCCTGGCCA	AGCTGTGGAG	TGCTGCCAAG	GGGACTGGTC	300
TAACAGGAAC	ATCACGGCCC	AGCTGCCAC	TAAAGGAAAA	TCCTTCCCTG	GAACACAGAA	360
TTTCCACTTG	GACGTTGGCC	TCATTATCCT	CTCTGTAGTG	TTCCAGTAT	GTCTTTAGC	420
CTGCCTGCTG	GGAGTTGCTC	TCCGAAAATT	TAAAAGGGCG	AACCAAGAAC	GCCTCAATCC	480
CCGAGACGTG	GAGTATGGCA	CTATCGAGGG	GCTCATCACC	ACCAATGTGG	GAGACAGCAC	540
TTTACGAGAT	TTATTGGATC	ATTCGTGTAC	ATCAGGAAGT	GGCTCTGGTC	TTCTTTCT	600
GGTACAAAGA	ACAGTGGCTC	GCCAGATTAC	ACTGTTGGAG	TGTGTGGGA	AAGGCAGGTA	660
TGGTGAGGTG	TGGAGGGGCA	GCTGGCAAGG	GGAAAATGTT	GCCGTGAAGA	TCCTCTCCTC	720
CCGTGATGAG	AAGTCATGGT	TCAGGGAAAC	GGAAATTGTAC	AAACACTGTCA	TGCTGAGGCA	780
TGAAAATATC	TTAGGTTTCA	TTGCTTCAGA	CATGACATCA	AGACACTCCA	GTACCCAGCT	840
GTGGTTAATT	ACACATTATC	ATGAAATGGG	ATCGTTGTAC	GACTATCTTC	AGCTTACTAC	900
TCTGGATACA	GTAGCTGTC	TTGGAATAGT	GCTGTCATA	GCTAGTGGTC	TTGCCACATT	960
GCACATAGAG	ATATTTGGCA	CCCAAGGGAA	ACCAGCCATT	GCCCACATCGAG	ATTTAAGAG	1020

CAAAAATACT CTGGTTAAGA AGAATGGACA GTGTTGCATA GCAGATTGG GCCTGGCAGT 1080  
 CATGCATTCC CAGAGCACCA ATCAGCTTGA TGTGGGGAAC AATCCCCGTG TGGGCACCAA 1140  
 GCGCTACATG GCCCCCCGAAG TTCTAGATGA ACCCATCCAG GTGGATTGTT TCGATTCTTA 1200  
 TAAAAGGGTC GATATTTGGG CCTTTGGACT TGTTTGTGG GAAGTGGCCA GGCGGATGGT 1260  
 GAGCAATGGT ATAGTGGAGG ATTACAAAGCC ACCGTTCTAC GATGTGGTTC CCAATAACCC 1320  
 AACTTTGAA GATATGAGGA AGGTAGTCTG TGTGGATCAA CAAAGGCCAA ACATACCCAA 1380  
 CAGATGGTTC TCAGACCCGA CATTAAACCTC TCTGGCCAAG CTAATGAAAG AATGCTGGTA 1440  
 TCAAAATCCA TCCGCAAGAC TCACAGCACT GCGTATCAA AAGACTTGA CCAAAATTGA 1500  
 TAATTCCTC GACAAATTGA AACTGACTG TTGACATT 1539

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 509 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

Met	Val	Asp	Gly	Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala
-25									-20					-15
Leu	Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro
-10									-5					1
Lys	Leu	Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu
5									10					15
Asp	His	Cys	Glu	Gly	Gln	Gln	Cys	Phe	Ser	Ser	Leu	Ser	Ile	Asn
20								25						30
Asp	Gly	Phe	His	Val	Tyr	Gln	Lys	Gly	Cys	Phe	Gln	Val	Tyr	Glu
35								40						45
Gln	Gly	Lys	Met	Thr	Cys	Lys	Thr	Pro	Pro	Ser	Pro	Gly	Gln	Ala
50								55						60
Val	Glu	Cys	Cys	Gln	Gly	Asp	Trp	Cys	Asn	Arg	Asn	Ile	Thr	Ala
65								70						75
Gln	Leu	Pro	Thr	Lys	Gly	Lys	Ser	Phe	Pro	Gly	Thr	Gln	Asn	Phe
80								85						90
His	Leu	Glu	Val	Gly	Leu	Ile	Ile	Leu	Ser	Val	Val	Phe	Ala	Val
95									100					105

Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val	Ala	Leu	Arg	Lys	Phe	Lys	
110							115				120				
Arg	Arg	Asn	Gln	Glu	Glu	Arg	Leu	Asn	Pro	Arg	Asp	Val	Glu	Tyr	Gly
125							130				135				
Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly	Asp	Ser	Thr	Leu	
140						145				150					
Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser	Gly	Ser	Gly	
155							160				165				
Leu	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile	Thr	Leu	
170							175				180				
Leu	Glu	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	
185							190				195				
Ser	Trp	Gln	Gly	Gly	Asn	Val	Ala	Val	Lys	Ile	Leu	Ser	Ser	Arg	
200							205				210				
Asp	Glu	Lys	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	
215							220				225				
Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	
230							235				240				
Thr	Ser	Arg	His	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	
245							250				255				
His	Glu	Met	Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	
260							265				270				
Asp	Thr	Val	Ser	Cys	Leu	Arg	Ile	Val	Leu	Ser	Ile	Ala	Ser	Gly	
275							280				285				
Leu	Ala	His	Leu	His	Ile	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Pro	
290							295				300				
Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Thr	Leu	Val	Lys	
305							310				315				
Lys	Asn	Gly	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Met	
320							325				330				
His	Ser	Gln	Ser	Thr	Asn	Gln	Leu	Asp	Val	Gly	Asn	Asn	Pro	Arg	
335							340				345				
Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Gly	Thr	
350							355				360				

Ile	Gln	Val	Asp	Cys	Phe	Asp	Ser	Tyr	Lys	Arg	Val	Asp	Ile	Trp
365														375
Ala	Phe	Gly	Leu	Val	Leu	Trp	Glu	Val	Ala	Arg	Arg	Met	Val	Ser
380														390
Asn	Gly	Ile	Val	Gly	Asp	Tyr	Lys	Pro	Pro	Phe	Tyr	Asp	Val	Val
395														405
Pro	Asn	Asn	Pro	Ser	Phe	Glu	Asp	Met	Arg	Lys	Val	Val	Cys	Val
410														420
Asp	Gln	Gln	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Phe	Ser	Asp	Pro
425														435
Thr	Leu	Thr	Ser	Leu	Ala	Lys	Leu	Met	Lys	Glu	Cys	Trp	Tyr	Gln
440														450
Asn	Pro	Ser	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu
455														465
Thr	Lys	Ile	Asp	Asn	Ser	Leu	Asp	Lys	Leu	Lys	Thr	Asp	Cys	
470														480

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1596 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCACGAGGAG	GGAGCCACGG	CCAGCGGTG	TAACACTTCA	TGGCTCTTAC	TCCACCTCTC	60
TTGCTCCCTCT	CTGAAGGGAC	CATGACCTTG	GGCTCCCCCA	GGAAAGGCCCT	TCTGATGCTG	120
CTGATGGCCT	TGGTGACCCA	GGGAGACCCCT	GTGAAGCCGT	CTCGGGGGCCC	GCTGGTGACC	180
TGCACGTGTG	AGAGCCCACA	TTGCAAGGGG	CCTACCTGCC	GGGGGGCCTG	GTGCACAGTA	240
GTGCTGGTGC	GGGAGGGAGGG	GAGGCACCCC	CAGGAACATC	GGGGCTGCCGG	GAACTTGCAC	300
ACGGGAGCTCT	GCAGGGGGCG	CCCCACCGAG	TTCGTCAACC	ACTACTGCTG	CGACAACAC	360
CTCTGCAACC	ACAAACGTGTC	CCTGGTGCCTG	GAGGCCACCC	AACCTCCTTC	GGACCAACCG	420
GGAACAGATG	CCCAGCTGGC	CCTGATCCTG	GGCCCCGTGC	TGGCCTTGCT	GGCCCTGGTC	480

GCCCTGGGTG	TCCTGGGCCT	GTGGCATGTC	CGACGGAGGC	AGGAGAAGCA	CGGTGACCTG	540
CACAGCGAGC	TGGGAGAGTC	CAGTCTCATC	CTGAAAGCAT	CTGAGCAGGA	CGACACCATG	600
TTGGGGGACC	TCCTGGACAG	TGACTGCACC	ACAGGGAGTG	GCTCAGGGCT	CCCCTTCCTG	660
GTGCAGAGGA	CAGTGGCACG	GCAGGTTGCC	TTGGTGGAGT	GTGTGGAAA	AGGCCGCTAT	720
GGCGAAGTGT	GGCGGGGCTT	GTGGCACGGT	GAGAGTGTGG	CCGTCAAGAT	CTTCTCCTCG	780
AGGGATGAAC	AGTCCTGGTT	CCGGGAGACT	GAGATCTATA	ACACAGTGTG	GCTCAGACAC	840
GACAACATCC	TAGGCTTCAT	CGCCTCAGAC	ATGACCTCCC	GCAACTCGAG	CACCGCAGCTG	900
TGGCTCATCA	CCGCACTACCA	CGAGCACGGC	TCCCTCTACG	ACTTTCTGCG	GAGACAGACG	960
CTGGAGCCCC	ATCTGGCTCT	GAGGCTAGCT	GTGTCCCGGG	CATGCGGCCT	GGCGCACCTG	1020
CACCGTGGAGA	TCTTTGGTAC	CACAGGGCAA	CCAGCCATTG	CCCACCGCGA	CTTCAAGAAC	1080
CGCAATGTGC	TGGTCAAGAG	CAACCTGCAG	TGTTGCATCG	CCGACCTGGG	CCTGGCTGTG	1140
ATGCACTCAC	AGGGCAGCGA	TTACCTGGAC	ATCGGCAACA	ACCCGAGAGT	GGGCACCAAG	1200
CGGTACATGG	CACCCGAGGT	GCTGGACCGAG	CAGATCCGCA	CGGACTGCTT	TGAGTCCTAC	1260
AAGTGGACTG	ACATCTGGC	CTTGGCCTG	GTGCTGTGGG	AGATTGCCCCG	CCGGACCATC	1320
GTGAATGGCA	TCGTGGAGGA	CTATAGACCA	CCCTTCTATG	GTGTGGTCCC	CAATGACCCCG	1380
AGCTTTGAGG	ACATGAAGAA	GGTGGTGTGT	GTGGATCAGC	AGACCCCCAC	CATCCCTAAC	1440
CGGCTGGCTG	CAGACCCGGT	CCTCTCAGGC	CTAGCTCAGA	TGATGCGGGG	GTGCTGGTAC	1500
CCAAACCCCT	CTGCCCCACT	CAACCGCCTG	CGGATCAAGA	AGACACTACA	AAAAATTAGT	1560
AACAGTCCAG	AGAAGCCCAA	AGTGATTCAAC	TAGCCCC			1596

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 503 AMINO ACIDS
  - (B) TYPE: AMINO ACID
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Leu	Gly	Ser	Pro	Arg	Lys	Gly	Leu	Leu	Met			
-20											-10			
Ala	Leu	Val	Thr	Gln	Gly	Asp	Pro	Val	Lys	Pro	Ser	Arg	Gly	Pro
-5												5		
Leu	Val	Thr	Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Gly	Pro	Thr
10														10
Cys	Arg	Gly	Ala	Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Glu	Gly
25														25
														30
														35

Arg	His	Pro	Gln	Glu	His	Arg	Gly	Cys	Gly	Asn	Leu	His	Arg	Glu
40					45					50				
Leu	Cys	Arg	Gly	Arg	Pro	Thr	Glu	Phe	Val	Asn	His	Tyr	Cys	Cys
55						60				65				
Asp	Asn	His	Leu	Cys	Asn	His	Asn	Val	Ser	Leu	Val	Leu	Glu	Ala
70						75				80				
Thr	Gln	Pro	Pro	Ser	Glu	Gln	Pro	Gly	Thr	Asp	Gly	Gln	Leu	Ala
85					90				95					
Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	Leu	Ala	Leu	Val	Ala	Leu
100					105				110					
Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg	Arg	Arg	Gln	Glu	Lys	Gln
115					120				125					
Arg	Asp	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	Ser	Leu	Ile	Leu	Lys
130					135				140					
Ala	Ser	Glu	Gln	Asp	Asp	Ser	Met	Leu	Gly	Asp	Leu	Leu	Asp	Ser
145					150				155					
Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln
160					165				170					
Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	Lys
175					180				185					
Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	Ser
190					195				200					
Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe
205					210				215					
Arg	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn
220					225				230					
Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser
235					240				245					
Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu
250					255				260					
Tyr	Asp	Phe	Leu	Arg	Arg	Gln	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu
265					270				275					
Arg	Leu	Ala	Val	Ser	Ala	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val
280					285				290					

Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp  
295 300 305  
Phe Lys Asn Arg Asn Val Leu Val Lys Ser Asn Leu Gln Cys Cys  
310 315 320  
Ile Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Gly Ser Asp  
325 330 335  
Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr  
340 345 350  
Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp Cys Phe  
355 360 365  
Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val Leu  
370 375 380  
Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp  
385 390 395  
Tyr Arg Pro Pro Phe Tyr Gly Val Val Pro Asn Asp Pro Ser Phe  
400 405 410  
Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr  
415 420 425  
Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala  
430 435 440  
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu  
445 450 455  
Asn Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser  
460 465 470  
Pro Glu Lys Pro Lys Val Ile His  
475 480

WHAT IS CLAIMED IS:

1. An isolated polynucleotide selected from the groups consisting of:
  - (a) a polynucleotide encoding for the TAR-1 polypeptide having the deduced amino acid sequence of Figure 1 or a fragment, analog or derivative of said polypeptide;
  - (b) a polynucleotide encoding for the TAR-3 polypeptide having the deduced amino acid sequence of Figure 2 or a fragment, analog or derivative of said polypeptide;
  - (c) a polynucleotide encoding for the TAR-1 polypeptide having the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. 75843 or a fragment, analog or derivative of said polypeptide;
  - (d) a polynucleotide encoding for the TAR-3 polypeptide having the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. 75842 or a fragment, analog or derivative of said polypeptide.
2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.
3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.
4. The polynucleotide of Claim 1 wherein the polynucleotide is genomic DNA.
5. The polynucleotide of Claim 2 wherein said polynucleotide encodes for TAR-1 having the deduced amino acid sequence of Figure 1.
6. The polynucleotide of Claim 2 wherein said polynucleotide encodes for TAR-3 having the deduced amino acid sequence of Figure 1.
7. The polynucleotide of Claim 2 wherein said polynucleotide encodes for the TAR-1 polypeptide encoded by the cDNA(s) of ATCC Deposit No. 75843.

8. The polynucleotide of Claim 2 wherein said polynucleotide encodes for the TAR-3 polypeptide encoded by the cDNA(s) of ATCC Deposit No. 75842.
9. The polynucleotide of Claim 1 having the coding sequence for TAR-1 as shown in Figure 1.
10. The polynucleotide of Claim 1 having the coding sequence for TAR-3 as shown in Figure 2.
11. The polynucleotide of Claim 2 having the coding sequence for TAR-1 deposited as ATCC Deposit No. 75843.
12. The polynucleotide of Claim 2 having the coding sequence for TAR-3 deposited as ATCC Deposit No. 75843.
13. A vector containing the DNA of Claim 2.
14. A host cell genetically engineered with the vector of Claim 13.
15. A process for producing a polypeptide comprising: expressing from the host cell of Claim 14 the polypeptide encoded by said DNA.
16. A process for producing cells capable of expressing a polypeptide comprising genetically engineering cells with the vector of Claim 13.
17. An isolated DNA hybridizable to the DNA of Claim 2 and encoding a polypeptide having TAR-1 activity.
18. An isolated DNA hybridizable to the DNA of Claim 2 and encoding a polypeptide having TAR-3 activity.
19. A polypeptide selected from the group consisting of (i) a TAR-1 polypeptide having the deduced amino acid sequence of Figure 1 and fragments, analogs and derivatives thereof and (ii) a TAR-3 polypeptide having the deduced amino acid sequence of Figure 2 and fragments, analogs and derivatives thereof, (iii) a TAR-1 polypeptide encoded by the cDNA of ATCC Deposit No. 75843 and fragments, analogs and derivatives of said polypeptide; and (iv) a TAR-3 polypeptide encoded by the cDNA of ATCC Deposit No. 75842 and fragments, analogs and derivatives of said polypeptide.

20. The polypeptide of Claim 19 wherein the polypeptide is TAR-1 having the deduced amino acid sequence of Figure 1.

21. The polypeptide of Claim 19 wherein the polypeptide is TAR-3 having the deduced amino acid sequence of Figure 2.

22. An antibody against the polypeptide of Claim 19.

23. A compound which inhibits activation of the polypeptide of Claim 19.

24. A compound which activates the polypeptide of claim 19.

25. A method for the treatment of a patient having need to activate TAR-1 comprising: administering to the patient a therapeutically effective amount of the compound of Claim 24.

26. A method for the treatment of a patient having need to activate TAR-3 comprising: administering to the patient a therapeutically effective amount of the compound of Claim 24.

27. A method for the treatment of a patient having need to inhibit TAR-1 comprising: administering to the patient a therapeutically effective amount of the compound of Claim 23.

28. A method for the treatment of a patient having need to inhibit TAR-3 comprising: administering to the patient a therapeutically effective amount of the compound of Claim 23.

29. The polypeptide of Claim 19 wherein the polypeptide is a soluble fragment of the TAR-1 receptor and is capable of binding a ligand for the receptor.

30. The polypeptide of Claim 19 wherein the polypeptide is a soluble fragment of the TAR-3 receptor and is capable of binding a ligand for the receptor.

31. A process for identifying antagonists and agonists to a TAR receptor comprising:  
preparing cells for expression of the receptor;  
contacting the cell with a receptor ligand and a compound to be screened;  
determining the signal generated by the cell in response to binding of the ligand; and  
identifying antagonists or agonists to the receptor.
32. A process for detecting cancer or the susceptibility to cancer by determining in a sample derived from a host the level of TAR-1 and TAR-3 receptors, whereby an elevated level indicates a cancer or the susceptibility to cancer.

## FIG. 1A

1 TACAATGGTAGATGGAGTGTGATTGATCCTTCCTGTGCTTATC  
 41 M V D G V M I L P V L I  
 13 M I A L P S M E D E K P K V N P K L  
 101 TACATGTGTGTGTGAAGGGCAAGGCCAACCCAAACTC  
 33 Y M C V C E G L S C G N E D H C E G Q Q  
 161 TGCTTTCCCTCACTGAGCATCAACGATGGCTTCCACGTCTACCGAAAGGCTGCCTCCAG  
 53 C F S S L S I N D G F H V Y Q K G C F Q  
 221 GTTTATGAGCAGGGAAAGATGACCTGTAAGAACCCCCGGCGTCCCCTGCCAAGCTGTGAG  
 73 V Y E Q G K M T C R T P P S P G Q A V E  
 281 TGCTGCCAAGGGGACTGGTGTAAACAGGAACATCACGGCCAGCTGCCACTAAAGGAAA  
 93 C C Q G D W C N R N I T A Q L P T K G K  
 341 TCCTCCCTGGAACACAGAAATTCCACTGGAGGTGGCCTCATTATCCTCTGTAGTG  
 113 S F P G T Q N F H L E V G L I I I S V V  
 401 TTGGCAGTATGTCCTTTAGCCTGCTGGAGTTGCTCTGGAAATT  
 133 F A V C L L A C L L G V A L R K F K R R  
 461 AACCAAAGGCCCTCAATCCCCGAGACGTGGAGTATGGCACTATCGAGGGCTCATCACC  
 153 N Q E R L N P R D V E Y G T I E G L I T  
 521 ACCAATGTGGAGACAGCACTTGGAGATTGGATCATTCGTGTACATCAGGAAGT  
 173 T N V G D S T L A D L L D H S C T S G S  
 581 GGCTCTGGTCTTCCTTCTGGTACAAGAACAGTGGCTGCCAGATTACACTGTTGGAG  
 193 G S G L P F L V Q R T V A R Q I T L L E  
 641 TGTGTGGAAAGGCAGGTATGGTGGAGGGCAGCTGGCAAGGGAAAATGTT  
 213 C V G K G R Y G E V W R G S W Q G E N V  
 701 GCCGTGAAGGATCCTCCCGTGTGAGGAAGTCACTGGAAACGGGAATTGTAC  
 233 A V K I L S S R D E K S W F R E T E L Y  
 761 AACACTGTGATGGCTGAGGGCATGAAAATATCTTAGGTTCATGCTTCAGACATGACATCA

MATCH WITH FIG. 1B

2 / 7

## MATCH WITH FIG. 1A

## FIG. 1B

N T V M L R H E N I L G F I A S D M T S  
 AGACACTCCAGTACCCAGCTGGTTAATTACACATTATCATGAAATGGGATCGGTGTCAC  
 R H S S T Q L W L I T H Y H E M G S L Y  
 GACTATCTCAGCTTACTACTCTGGATAACAGTAGCTGCTTCAATAATGCTGCTGCCATA  
 D Y L Q L T T L D T V S C L R I V L S I  
 GCTAGTGGTCTGCACATTGACATAGAGATATTGGCACCCAAAGGGAAACCAGCCATT  
 A S G L A H L H I E I F G T Q G K P A I  
 GCCCATCGAGATTAAAGGCAAAATACTCTGGTTAAGGAAGAATGGACAGTGTGGCATA  
 A H R D L K S K N T L V K N G Q C C I  
 GCAGATTGGCCCTGGCAGTCATGCATTCCCAGAGCACCAATCAGCTGATGTGGGAAC  
 A D L G L A V M H S Q S T N Q L D V G N  
 ATCCCCGCTGGCCACCAAGGGCTACATGGCCCCGAAAGTTCTAGATGAAACCATCCAG  
 N P R V G T K R Y M A P E V L D E T I Q  
 GTGGATTGTTTCGATTCTTATAAAAGGGTGCATATTGGCCTTTGGACTTGTGTTGCG  
 V D C F D S Y K R V D I W A F G L V L W  
 GAAGTGGCCAGGGGATGGTGAAGCAATGGTATAAGTGGAGGATTACAAGGCCACCGTTCTAC  
 E V A R R M V S N G I V E D Y K P P F Y  
 GATGTTCCCAAATAACCCAAAGTTGAAGATATGACGAAGGTAGTCTGTGGGATCAA  
 D V V P N N P S F E D M R K V V C V D Q  
 CAAAGGCCAACATACCCAAACAGATGGTCTCAGACCCGACATTAACCTCTGGCCAAAG  
 Q R P N I P N R W F S D P T L T S L A K  
 CTAATGAAAGAATGCTGGTATCAAAATCCATCGCAAGGACTCACAGGACTGGGTATCAA  
 L M K E C W Y Q N P S A R L T A L R I K  
 AAGACTTTGACCAAAATTGATAATTCCCTCGACAAATGAAAATGACTGTTGACATT  
 K T L T K I D N S L D K T D C \*

FIG. 2A

1 GCACGAGGGAGGCCACGGCCAGGGACCATGAACTCTCTGCTTACTCCACCTCTC  
 61 TTGCTCCTCTCTGAAGGGACCATGACCTTGGCTCCCCCAGGAAAGGCCTTCTGATGCTC  
 121 CTCGATGGCCTTGGTACCCAGGGAGGACCTTGTCAAGGCCCTTGTCTGATGCTC  
 141 L W A L V T Q G D P V K P S R G P L M L  
 181 TGCACCGTGTGAGAGCCCACATTGCAAGGGCCTAACCTGGGGGGGGCTGGTGACC  
 341 C T C E S P H C K G P T C R G A W C T V  
 241 GTGCTGGTGGGGAGGGAGGGACCCAGGAAACATGGGGCTGGTGGCACAGTA  
 541 V L V R E E G R H P Q E H R G C G N L H  
 301 AGGGAGGCTCTGCAAGGGGGCCCCACCGAGTTGCTCAACCAACTACTGGCTGGCAC  
 741 R E L C R G R P T E F V N H Y C C D N H  
 361 CTCTGCAACACAACGTCGTCCTGGCTGGGGCACCCAAACCTCCTGGAGCAACCG  
 941 L C N H N V S L V L E A T Q P P S E Q P  
 421 CGAACAGATGGCCAGCTGGCCCTGATCCTGGCCCCCTGGCTGGCCCTGGAGCAACCG  
 114 G T D G Q L A L I L G P V L A L A L V  
 481 GCCCTGGGTCTGGGCTTGTGGCATGTCGGCATGGGAGGGCAGGGAGGAGGAGG  
 134 A L G V L G L W H V R R R Q E X Q R D L  
 541 CACAGGGAGCTGGGAGAGTCCAGTCTCATCCCTGAAAGCATCTGAGGAGGAGGAGG  
 154 H S E L G E S S L I L K A S E Q D D S M  
 601 TTGGGGACCTCCTGGACAGTGAATGACCCAGGGAGTGGCTCAGGGCTCCCTTCTG  
 174 L G D L L D S D C T T G S G S G L P F L  
 661 GTGGAGGGACAGTGGCACGGCAGGGTGGCTTGGGAAAGATCTTCTGCTCAGGGCT  
 194 V Q R T V A R Q V A L V E C V G K G R Y  
 721 GGGCAAGTGTGGGGGCTTGTGGCACGGTGAAGACTGTGGCTTGGGAAAGGCCGCTAT  
 214 G E V W R G L W H G E S V A V K I F S S  
 781 AGGGATGAACAGTCCCTGGTCCGGAGACTGAGATCTATAACACAGTGTGGCTCAGGACAC  
 234 R D E Q S W F R E T E I Y N T V L L R H  
 841 GACAAACATCCTAGGCTTCATGGCCTCAGACATGACCTCCCGGAAACTCGAGCAGGCTG

## MATCH WITH FIG. 2A

## FIG. 2B

254 D N I L G F I A S D M T S R N S S T Q L  
 901 TGGCTCATCACGGCACTACACCGAGCACCGGCTCCCTCTACGACTTCTGGGAGACAGACG  
 274 W L I T H Y H E H G S L Y D F L R R Q T  
 961 CTCGGAGCCCCATCTGGCTCTGAGGCTAGCTGTCCGGCAGATGGGCCTGGGGCACCTG  
 294 L E P H L A L R L A V S A A C G L A H L  
 1021 CACGTGGAGATCTTGGTACACGGCAAAACAGCCATTGCCAACCGGACTTCAAAGAAC  
 314 H V E I F G T Q G K P A I A H R D F K N  
 1081 CGGAATGTGCTGGTCAAGGAGCAACCTGGCAAGTGTGCATGCCGACCTGGCCTGGCTGTG  
 334 R N V L V K S N L Q C C I A D L G L A V  
 1141 ATGGCACTACAGGGCAGCCATTACCTGGACATCGGCAACAAACCCCAGAGTGGGCACCAAG  
 354 M H S Q G S D Y L D I G N N P R V G T K  
 1201 CGGTACATGGCACCCGGAGGAGGAGGAGCTGGACAGATCCGCACGGACTGCTTGAGTCTAC  
 374 R Y M A P E V L D E Q I R T D C F E S Y  
 1261 AACTGGACTGACATCTGGGCCTTGGCTGGAGATTGCCGGACCATC  
 394 K W T D I W A F G L V L W E I A R R T I  
 1321 GTGAATGGCATCGTGGAGGACTATAGACCAACCCCTCTATGGTGTGCCAATGACCCC  
 414 V N G I V E D Y R P P F Y G V V P N D P  
 1381 AGCTTTGAGGACATGAAGAAGGTGGTGTGGATCAGCAGACCCCCACCATCCCTAAC  
 434 S F E D M K V V C V D Q Q T P T I P N.  
 1441 CGGCTGGCTGGAGACCCGGTCCCTCTCAGGCCTAGCTCAGATGATGGGGAGTGCTGGTAC  
 454 R L A A D P V L S G L A Q M M R E C W Y  
 1501 CCAAACCCCTCTGGCCGACTCAACGGCCTGGGATCAAGAAGACACTACAAAAATTAGT  
 474 P N P S A R L N A L R I K T L Q K I S  
 1561 AACAGTCCAGAGAAGCCCCAAAGTCATTCACTAGCCC  
 494 N S P E K P K V I H \*

5 / 7

## FIG. 3A

1	M V D G V M I I L P V L I M . I A L P S P S M E D E K P K V N P	TAR-1
1	M T L G S P R K G L L M L L M A L V T Q G D P V K P S R G P	TAR-3
1	M E A A S A A L R R C L L I V L Y A A A T L L L - - - P G A	TGF-beta receptor
31	K L Y M C V C E G L S C G N E D - H C E G Q - Q C F S S L S	TAR-1
31	- L V T C T C E S P H C - K G P - T C R G A - W C T V V I L V	TAR-3
28	R K A L Q C F C H - - L C T K D N . F T C E T D G L C F V S V T	TGF-beta receptor
59	I N D G F H V Y - Q K G C F Q - - - - V Y E Q G K M T C K T	TAR-1
57	R E G R H P Q E H R G C G N - - - - L H R E - - - L C R G	TAR-3
56	- E T T D K V I H N S M C I A E I D L I P R D R P F V C A P	TGF-beta receptor
84	P P S P P G Q A V E C C Q G D W C N R N I T A Q L P T K G K S	TAR-1
80	R P T E F V N H Y C C D N H L C N H N V S L V L E A T Q P P	TAR-3
85	S S K T G A V T Y C C N Q D H C N K - - - I E L P T T G P F	TGF-beta receptor
114	F - - P G T Q N F H L E V G L I I L S V V F A Y C L L A C L	TAR-1
110	S E Q P G T D G - - - Q L A L I - L G P V L A L L A L V A L	TAR-3
112	S E K Q S A G L G P V E L A A V T A G P V C F V C I - - -	TGF-beta receptor
142	L G V A L R K F K R R N Q E R L N P R D V E Y G T I E - G L	TAR-1
136	G V L G L W H V R R - Q E K Q R D L H S E L G E S S L I L	TAR-3
138	- A L M V Y I C H N R T V I H H R V P N E E D P S L D - - -	TGF-beta receptor
171	I T T N V G D S T L A D L L D H S C T S G S G L P F L V	TAR-1
165	K A S E Q D D S M L G D L L D S D C T T G S G S G L P F L V	TAR-3
166	R P F I S E G T T L K D L I Y D M T T S G S G L P L L V	TGF-beta receptor

MATCH WITH FIG. 3B

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## MATCH WITH FIG. 3A

## FIG. 3B

201	Q R T V A R Q I T L L E C V G K G R Y G E V W R G S W Q G E TAR-1
195	Q R T V A R Q V A L V E C V G K G R Y G E V W R G L W H G E TAR-3
196	Q R T I A R T T V I L Q E S T I G K G R F G E V W R G K W R G E TGF-beta receptor
231	N V A V K I L S S R D E K S W F R E T E L Y N T V M L R H E TAR-1
225	S V A V K I F S S R D E Q S W F R E T E I Y N T V L L R H D TAR-3
226	E V A V K I F S S R E E R S W F R E A E I Y Q T V M L R H E TGF-beta receptor
261	N I L G F I A S D M T S R H S S T Q L W L I T H Y H E M G S TAR-1
255	N I L G F I A S D M T S R N S S T Q L W L I T H Y H E H G S TAR-3
256	N I L G F I A A D N K D M G T W T O L W L V S D Y H E H G S TGF-beta receptor
291	L Y D Y L Q J T T L D T V S C I R I V L S I A S G L A H L H TAR-1
285	L Y D F L R [K] Q T I E P H L A L V S A A C G L A H L H TAR-3
286	L F D Y L N R Y T V T V E G M I K L A L S T A S G L A H L H TGF-beta receptor
321	I E I F G T Q G K P A I A H R D L K S K N T L V K K N G Q C TAR-1
315	V E I F G T Q G K P A I A H R D F K N R N V L V K S N L O C TAR-3
316	M E I V G T Q G K P A I A H R D L K S K N I L V K K N G T C TGF-beta receptor
351	C I A D L G L A V M H S Q S T N Q L D V G N N P R V G T K R TAR-1
345	C I A D L G L A V M H S Q G S D Y L D I G N N P R V G T K R TAR-3
346	C I A D L G L A V R H D S A T D T I D I A P N H R V G T K R TGF-beta receptor
381	Y M A P E V L D E T I Q V D C F D S Y K R V D I W A F G L V TAR-1
375	Y M A P E V L D E Q I R T D C F E S X K W T D I W A F G L V TAR-3
376	Y M A P E V L D D S I N M K H F E S F K R A D I Y A M G L V TGF-beta receptor

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MATCH WITH FIG. 3C

7 / 7

## MATCH WITH FIG. 3B

## FIG. 3C

411	L W E V A R R M V S N G I V E D Y K P P F Y D V V P N N P S	TAR-1
405	L W E I A R R T I V N G I V E D Y R P P F Y G Y V P N D P S	TAR-3
406	F W E I A R R C S I G G I H E D Y Q L P P Y Y D L V P S D P S	TGF-beta receptor
441	F E D M R K V V C V D Q Q P N R P N I P N R W F S D P T L T S L	TAR-1
435	F E D M R K V V C V D Q Q T P T I P N R L A A D P V L S G L	TAR-3
436	V E E M R K V V C E Q K L R P N I P N R W Q S C E A L R V M	TGF-beta receptor
471	A K L M K E C W Y Q N P S A R L T A L R I K K T L T K I D N	TAR-1
465	A Q M M R E C W Y P N P S A R L N A L R I K K T L Q K I S N	TAR-3
466	A K I M R E C W Y A N G A A R L T A L R I K K T L S Q L S Q	TGF-beta receptor
501	S L D K L K T D C	TAR-1
495	S P E K P K V I H	TAR-3
496	Q - E G I K M	TGF-beta receptor

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/11328

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.

US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 70.1, 70.3, 71.1, 172.1, 172.3, 240.2, 320.1; 530/300, 350; 536/23.1, 23.5, 24.31

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched  
Sequence Databases: EMBL, GenBankElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
APS; STN files: Biosis, Medline, EMBASE, CA, WPI/DS  
search terms: activin; activin(with)receptor(s)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category <sup>a</sup>	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Oncogene, Vol. 8, Number 10, issued 1993, P. ten Dijke et al., "Activin Receptor-like Kinases: A Novel Subclass of Cell-surface Receptors with Predicted Serine/Threonine Kinase Activity", pages 2879-2887, see entire document, especially pages 2881-2882.	1-21, 29-30
Y	Cell, Vol. 75, issued 19 November 1993, L. Attisano et al., "Identification of Human Activin and Tgf $\beta$ Type I Receptors That Form Heteromeric Kinase Complexes with Type II Receptors", pages 671-680, see entire document.	1-21, 29-30

 Further documents are listed in the continuation of Box C. See patent family annex.

- <sup>b</sup> Special categories of cited documents:
- "A" document defining the general area of the art which is not considered to be of particular relevance
- "E" earlier document published on or after the international filing date
- "L" document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, e.g., exhibition or other event
- "P" document published prior to the international filing date but later than the priority date claimed
- "T" document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, and combination brings nothing new to a person skilled in the art
- "Z" document number of the main patent family

Date of the actual completion of the international search

12 FEBRUARY 1995

Date of mailing of the international search report

27 FEB 1995

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231  
Facsimile No. (703) 305-3230

Authorized officer

ARIE M. MICHELSON, PH.D.

Telephone No. (703) 308-0196

## INTERNATIONAL SEARCH REPORT

Int. application No.  
PCT/US94/11328

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Proc. Natl. Acad. Sci. USA, Vol. 90, issued December 1993, Tsuchida et al., "Cloning and Characterization of a Transmembrane Serine Kinase That Acts as an Activin Type I Receptor", pages 11242-11246, especially page 11243, Fig. 1.	1-21, 29-30
Y	Cell, Vol. 68, issued 10 January 1992, L. Attisano et al., "Novel Activin Receptors: Distinct Genes and Alternative mRNA Splicing Generate a Repertoire of Serine/Threonine Kinase Receptors", pages 97-108, see entire document.	1-21, 29-30
Y	Science, Vol. 260, issued 28 May 1993, R. Ebner et al., "Cloning of a Type I TGF- $\beta$ Receptor and Its Effect on TGF- $\beta$ Binding to the Type II Receptor", pages 1344-1348, see entire document.	1-21, 29-30
A	Cell, Vol. 68, issued 21 February 1992, H. Lin, et al., "Expression Cloning of the TGF- $\beta$ Type II Receptor, a Functional Transmembrane Serine/Threonine Kinase", pages 775-785, see entire document.	1-21, 29-30
Y	Cell, Vol. 65, issued 14 June 1991, L. Mathews et al., "Expression Cloning of an Activin Receptor, a Predicted Transmembrane Serine Kinase", pages 973-982, see entire document.	1-21, 29-30
Y	Science, Vol. 255, issued 27 March 1992, L. Mathews et al., "Cloning of a Second Type of Activin Receptor and Functional Characterization in <i>Xenopus</i> Embryos", pages 1702-1705, see entire document.	1-21, 29-30
Y	WO, A, 92/20793 (MATHEWS ET AL.) 26 November 1992, see entire document.	1-21, 29-30
Y	WO, A, 93/19177 (DONAHOE ET AL.) 30 September 1993, see entire document.	1-21, 29-30
Y	Developmental Dynamics, Vol. 196, issued 1993, W. He et al., "Developmental Expression of Four Novel Serine/Threonine Kinase Receptors Homologous to the Activin/Transforming Growth Factor- $\beta$ Type II Receptor Family", pages 133-142, see entire document.	1-21, 29-30

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/11328

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Journal of Biological Chemistry, Vol. 268, No. 17, issued 15 June 1993, K. Matsuzaki et al., "A Widely Expressed Transmembrane Serine/Threonine Kinase That Does Not Bind Activin, Inhibin, Transforming Growth Factor $\beta$ , or Bone Morphogenic Factor", pages 12719-12723, see entire document.	1-21, 29-30

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/11328

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3.  Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1.  As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-21, 29-30

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US94/11328

## A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C12N 5/00, 5/10, 5/16, 7/00, 7/01, 15/00, 15/09, 15/10, 15/11, 15/12, 15/63; C12P 21/00, 21/02; C07K 2/00, 14/00, 14/705, 14/71, 14/715; C07H 21/00, 21/04

## A. CLASSIFICATION OF SUBJECT MATTER: US CL :

435/69.1, 70.1, 70.3, 71.1, 172.1, 172.3, 240.2, 320.1; 530/300, 350; 536/23.1, 23.5, 24.31

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claims 1-21 and 29-30, drawn to polynucleotides and polypeptides, classified in U.S. Class 536, subclass 23.1; Class 435, subclass 69.1; Class 435, subclass 320.1; Class 530, subclass 350; Class 530, subclass 300.

Group II, claim 22, drawn to an antibody, classified in U.S. Class 530, subclass 389.1; Class 530, subclass 388.22.

Group III, claims 23-24, drawn to compounds, classification dependent on species.

Group IV, claims 25-28, drawn to methods of treatment, classification dependent on species.

Group V, claim 31, drawn to process for identifying antagonists and agonists, classified in U.S. Class 436, subclass 501.

Group VI, claim 32, drawn to process for detecting cancer or susceptibility to cancer, classification dependent on species employed in said process.

The inventions listed as Groups I-VI do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Groups I and II are related insofar as the polypeptides of claim 19 can be used as the antigens with which to generate the antibody of claim 22. However, the groups are distinct because the polypeptides of claim 19 can be used for a materially different purpose, such as to screen for ligands that bind to the polypeptides.

Groups I and III are related insofar as the polypeptides of group I can be used to screen for agonists and antagonists of the polypeptides. However, the groups are distinct because the polypeptides of group I can be used for a materially different purpose, such as for generating antibodies against the polypeptides for diagnostic, research or therapeutic purposes.

Groups I and IV are related only insofar as the compound of group IV can potentially be used therapeutically by virtue of their ability to bind the polypeptides of group I. However, the groups are distinct because the polypeptides of group I can be used for a materially different purpose, such as for generating antibodies against the polypeptides for diagnostic, research or therapeutic purposes.

Groups I and V are related insofar as the polypeptides of group I can be used to identify agonists or antagonists of the claimed receptors. However, the groups are distinct because the polypeptides of group I can be used for a materially different purpose, such as for generating antibodies against the polypeptides for diagnostic, research or therapeutic purposes.

Groups I and VI are related insofar as the amount of the polypeptides of group I present in a cell may be used as a diagnostic for cancer or susceptibility to cancer. However, the polypeptides of group I can be used for a materially different purpose, such as for generating antibodies against the polypeptides for diagnostic, research or therapeutic purposes.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US94/11328

Groups II and III are related only insofar as an antibody directed against the polypeptides of group I can in principle also serve as an agonist or antagonist of the polypeptides. However, the groups are distinct because no such limitation is recited in the claim, and as such: (i) the compounds of group III can comprise molecules that are physically and chemically distinct from the antibody of group II and (ii) the antibody of group II can be used for a materially different purpose, such as for detecting the presence of the polypeptides of group I in a cell or tissue.

Groups II and IV are related only insofar as the antibody of group II could in principle be used as the compounds claimed in group IV. However, the groups are distinct for the same reasons given with respect to groups II and III above.

Groups II and V are related only insofar as the antibody of group II could in principle be identified using the method of group V. However, the groups are clearly distinct because (i) the method of group V is a generic method not limited to detection of antibodies and (ii) the antibody of group II can be used for a materially different purpose, such as for detecting the presence of the polypeptides of group I in a cell or tissue.

Groups II and VI are related insofar as the antibody of group II could in principle be used as the diagnostic agent to be employed in the process of group VI. However, the claims of group VI do not contain this limitation, and furthermore, (i) the process of group VI can employ other agents, such as a radiolabelled ligand for use in a binding assay, and (ii) the antibody of group II can be used for a materially different purpose, such as in an affinity column to purify the polypeptides of group I.

Groups III and IV are related insofar as the methods of treatment of group IV employ the compounds of group III. However, the groups are distinct because the compounds of group III can be used for materially different purposes, such as in the production of radiolabelled ligands for use in binding assays to detect levels of the polypeptides of group I.

Groups III and V are related only insofar as the compounds of group III may be detected using the method of group V. However, the groups are distinct because the compounds of group III can be used for materially different purposes, such as in the production of radiolabelled ligands for use in binding assays to detect levels of the polypeptides of group I. Furthermore, the compounds of group III can comprise a virtually infinite variety of molecules which could have a virtually infinite variety of materially different purposes, depending on the species of compound.

Groups III and VI are related insofar as at least some of the compounds of group III could in principle be used, for example in radiolabelled form, as the diagnostic agents in the process of group VI. However, the groups are distinct because the compounds of group III can comprise a virtually infinite variety of molecules which could have a virtually infinite variety of materially different purposes, depending on the species of compound.

Groups IV and VI are related only insofar as the methods of group IV employ compounds that interact with receptors whose levels are detected in the process of group VI. However, the groups are clearly distinct, as they are drawn to materially different methods with distinctly different objectives.

Groups V and VI are related insofar as at least some of the compounds identified using the method of group V could in principle be used, for example in radiolabelled form, as a diagnostic agent in the method of group VI. However, the groups are distinct because (i) the methods are materially distinct and have distinctly different (perhaps reciprocal) objectives and (ii) the compounds identified using the method of group V can be used for materially different purposes, for example, as a research tool to study structure-function relationships in TGF receptors.

Accordingly, the claims are not so linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.